GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2003, 07:51:53 ; Search time 2838 Seconds
(without alignments)
5342.693 Million cell updates/sec

Title: US-09-857-581-66
Perfect score: 2396
Sequence: 1 MLLELALGLXVLALFXHLRP.....AHSLVCVPLARIGVASKLLS 521

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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11
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
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36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2270	94.7	1563	8	AF195812	AF195812 Pisum sat
2	2269	94.7	1774	8	AF195798	AF195798 Glycine m
3	2268	94.7	1566	8	AF195806	AF195806 Vigna rad
4	2268	94.7	1566	8	AF195807	AF195807 Vigna rad
5	2268	94.7	1566	8	AF195808	AF195808 Vigna rad
6	2268	94.7	1566	8	AF195810	AF195810 Trifolium
7	2268	94.7	1566	8	AF195811	AF195811 Trifolium
8	2267	94.6	1566	8	AF195809	AF195809 Vigna rad
9	2267	94.6	1722	8	AF135484	AF135484 Glycine m
10	2251	93.9	1824	8	AF022462	AF022462 Glycine m
11	2251	93.9	1824	8	AF195799	AF195799 Glycine m
12	2201.5	91.9	1902	8	AF195819	AF195819 Glycine m
13	2189	91.4	1800	8	AF195818	AF195818 Glycine m
14	2183	91.1	1501	8	AF195801	AF195801 Medicago
15	2180	91.0	1501	8	AF195800	AF195800 Medicago
16	2179	90.9	1501	8	AF195815	AF195815 Trifolium

17	2178	90.9	1501	8	AF195802	AF195802 Medicago
18	2178	90.9	1501	8	AF195804	AF195804 Lens culi
19	2177	90.9	1500	8	AF195817	AF195817 Beta vulg
20	2177	90.9	1501	8	AF195805	AF195805 Lens culi
21	2177	90.9	1501	8	AF195813	AF195813 Lupinus a
22	2176	90.8	1501	8	AF195803	AF195803 Vicia vil
23	2174	90.7	1496	8	AF195814	AF195814 Trifolium
24	2168	90.5	1497	8	AF195816	AF195816 Beta vulg
25	2151	89.8	1809	8	AF462633	AF462633 Pueraria
26	2141	89.4	1929	8	AF089850	AF089850 Glycine m
27	1980.5	82.7	1895	8	AB023636	AB023636 Glycyrrhi
28	1957	81.7	1875	8	CAR243804	AJ243804 Cicer ari
29	1907	79.6	1557	8	AB024931	AB024931 Lotus jap
30	1227	51.2	1920	8	AB001380	AB001380 Glycyrrhi
31	1223	51.0	2010	8	AB022733	AB022733 Glycyrrhi
32	955.5	39.9	1685	8	AB028152	AB028152 Torenia h
33	955.5	39.9	1730	6	E52152	E52152 Gene encodi
34	954.5	39.8	1706	8	AB028151	AB028151 Antirrhin
35	954.5	39.8	1724	6	E52151	E52151 Gene encodi
36	943.5	39.4	1697	6	AX043769	AX043769 Sequence
37	943.5	39.4	1697	8	AF156976	AF156976 Gerbera h
38	932.5	38.9	1770	6	AX077832	AX077832 Sequence
39	932.5	38.9	1770	6	E52155	E52155 Gene encodi
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44	878	36.6	1659	8	GMC450CP5	Y10492 G.max mRNA
45	854	35.6	1829	8	D86351	D86351 Glycine max

ALIGNMENTS

RESULT 1
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LOCUS AF195812 1563 bp mRNA linear PLN 16-FEB-2000
DEFINITION Pisum sativum isoflavone synthase 1 (ifs1) mRNA, partial cds.
ACCESSION AF195812
VERSION AF195812.1 GI:6979547
KEYWORDS .
SOURCE Pisum sativum.
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
REFERENCE 1 (bases 1 to 1563)
AUTHORS Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and McGonigle,B.
TITLE Identification and expression of isoflavone synthase, the key enzyme for biosynthesis of isoflavones in legumes
JOURNAL Nat. Biotechnol. 18 (2), 208-212 (2000)
MEDLINE 20124255
PUBMED 10657130
REFERENCE 2 (bases 1 to 1563)
AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box 80402, Wilmington, DE 19880-0402, USA
FEATURES Location/Qualifiers
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gene 1. .>1563
/gene="ifs1"
CDS 1. .>1563
/gene="ifs1"
/note="cytochrome P450"
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YSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGAL
VLFNVWQVGKDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCP
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PLARIGVASKLLS"
BASE COUNT 399 a 414 c 379 g 371 t
ORIGIN

Alignment Scores:

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Score:	2270.00	Matches:	454
Percent Similarity:	87.14%	Conservative:	0
Best Local Similarity:	87.14%	Mismatches:	67
Query Match:	94.74%	Indels:	0
DB:	8	Gaps:	0

US-09-857-581-66 (1-521) x AF195812 (1-1563)

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Db       1 ATGTTGCTGGAACTTGCACTTGGTTTGTTTGTGTTAGCTTTGTTTCTGCACTTGCGTCCC 60

Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
           ||||||   |||   ||||||||||||||||||||||||||||||||||||||||   |||
Db      61 ACACCAAGCGCAAAATCAAAAGCACTTCGCCACCTCCCAAACCCTCCAAGCCCAAAGCCT 120

Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db     121 CGTCTTCCCTTCATTGGCCACCTTCACCTCTTAAAAGATAAACTTCTCCACTATGCACTC 180

Qy      61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
           ||||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db     181 ATCGATCTCTCCAAAAAGCATGGCCCCTTATTCTCTCTCCTTCGGCTCCATGCCAACC 240

Qy      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
           ||||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db     241 GTCGTTGCCTCCACCCCTGAGTTGTTCAAGCTCTTCCTCCAAGCCCACGAGGCAACTTCC 300
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Qy    101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
          |||   ||||||||||||||||||||   |||   ||||||||||||       ||||||
Db    301 TTCAGCACAAGGTTCCAAACCTCTGCCGTAAGACGCCTCACTTACGACAACTCTGTGGCC 360

Qy    121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
              |||   ||||||||||||   ||||||||||||||||||||||||||||||||||||
Db    361 ATGGTTCCATTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 420

Qy    141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
          ||||||||||||||||||   ||||||||||||||||||||||||||||||||   |||
Db    421 AACGCCACCACCGTCAACGAGCTCAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 480

Qy    161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
          |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||||
Db    481 AGGGTTATGGCCCAAAGCGCAGAGGCCCAGAAGCCCCTTGACGTCACCGAGGAGCTTCTC 540

Qy    181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
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Db    541 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 600

Qy    201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
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Db    601 ATCGCTCGCGAGGTCCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTGGCCT 660

Qy    221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTGAAGTATCTCAAGGTTGGAAAGTATGAGAAGAGGATTGATGACATCTTGAACAAGTTC 720

Qy    241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
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Db    721 GACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTCAGAAGGAGAAAGAAC 780

Qy    261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
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Qy    281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
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Qy    301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
              ||||||||||||   ||||||||||||      ||||||||||||||||||||||||
Db    901 TTTTTCTCTGCAGGGACAGATTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAGCTC 960

Qy    321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
          ||||||||||||   ||||||      ||||||||||||   ||||||||||||||||||||
Db    961 ATCAACAATCCCAGGGTGTTGCAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGCAAA 1020

Qy    341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
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Db   1021 GATAGACTCGTTGACGAAGTCGACACTCAAAACCTTCCTTACATTAGGGCCATTGTGAAG 1080

Qy    361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
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Qy    381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
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Qy    401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
          |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db   1201 GGAAAGGACCCCAAATACTGGGACAGACCATCAGAATTCCGTCCCGAGAGGTTCTTAGAA 1260

Qy    421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
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Db   1261 ACTGGCGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGCCAGCATTTCCAACTCCTC 1320

Qy    441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
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Qy    461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
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Db   1381 ACACTTCTTGCATCTCTTATCCAATGCTTTGACCTGCAAGTGCTGGGCCCTCAAGGACAA 1440

Qy    481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
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Db   1441 ATATTGAAAGGTGACGATGCCAAAGTTAGCATGGAAGAGAGAGCTGGCCTCACCGTTCCA 1500

Qy    501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
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Db   1501 AGGGCACATAGTCTCGTTTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1560

Qy    521 Ser 521
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Db   1561 TCT 1563
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RESULT 2
AF195798
LOCUS       AF195798               1774 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Glycine max isoflavone synthase 1 (ifs1) mRNA, complete cds.
ACCESSION   AF195798
VERSION     AF195798.1  GI:6979519
KEYWORDS    .
SOURCE      Glycine max.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 1774)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1774)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
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80402, Wilmington, DE 19880-0402, USA

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                     /db_xref="taxon:3847"
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BASE COUNT      485 a    445 c    406 g    438 t
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Alignment Scores:

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Percent Similarity:	87.14%	Conservative:	0
Best Local Similarity:	87.14%	Mismatches:	67
Query Match:	94.70%	Indels:	0
DB:	8	Gaps:	0

US-09-857-581-66 (1-521) x AF195798 (1-1774)

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Qy       1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
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Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
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Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
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Db     187 CGTCTTCCCTTCATTGGCCACCTTCACCTCTTAAAAGATAAACTTCTCCACTATGCACTC 246

Qy      61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
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Qy      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
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Qy     141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
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Db     487 AACGCCACCACCGTCAACAAGCTCAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 546

Qy     161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
           |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||||
Db     547 AGGGTTATGGCCCAAAGCGCAGAGGCCCAGAAGCCCCTTGACGTCACCGAGGAGCTTCTC 606

Qy     181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
           ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||
Db     607 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 666

Qy     201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
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Db     667 ATCGCTCGCGAGGTTCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTGGCCT 726

Qy     221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
           ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 TTGAAGTATCTCAAGGTTGGAAAGTATGAGAAGAGGATTGATGACATCTTGAACAAGTTC 786

Qy     241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
           ||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db     787 GACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTCAGAAGGAGAAAGAAC 846

Qy     261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
           ||||||      |||||||||   |||||||||   ||||||||||||||||||||||||
Db     847 GGAGAAGTTGTTGAGGGCGAGGCCAGCGGCGTCTTCCTCGACACTTTGCTTGAATTCGCT 906

Qy     281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
           ||||||||||||   ||||||||||||||||||      ||||||||||||||||||||||
Db     907 GAGGACGAGACCATGGAGATCAAAATTACCAAGGAGCAAATCAAGGGCCTTGTTGTCGAC 966

Qy     301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
               ||||||||||||   ||||||||||||      ||||||||||||||||||||||||
Db     967 TTTTTCTCTGCAGGGACAGATTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAGCTC 1026

Qy     321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
           ||||||||||||   ||||||      ||||||||||||   ||||||||||||||||||
Db    1027 ATCAACAATCCCAGGGTGTTGCAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGCAAA 1086

Qy     341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
           |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1087 GATAGACTCGTTGACGAAGTTGACACTCAAAACCTTCCTTACATTAGGGCCATTGTGAAG 1146

Qy     361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
           ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db    1147 GAGACATTCCGAATGCACCCACCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1206

Qy     381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
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Db   1207 GAGATTAATGGGTATGTGATCCCAGAGGGAGCATTGGTTCTTTTCAATGTTTGGCAAGTA 1266

Qy    401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
          |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db   1267 GGAAGGGACCCCAAATACTGGGACAGACCATCAGAATTCCGTCCCGAGAGGTTCTTAGAA 1326

Qy    421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
          |||   ||||||||||||||||      ||||||||||||||   ||||||||||||||
Db   1327 ACTGGTGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGCCAGCATTTCCAACTCCTC 1386

Qy    441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
          ||||||||||||||||||   ||||||||||||||   ||||||||||||||   |||
Db   1387 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGTGTCAATTTGGCTACTTCAGGAATGGCA 1446

Qy    461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1447 ACACTTCTTGCATCTCTTATCCAATGCTTTGACCTGCAAGTGCTGGGCCCTCAAGGACAA 1506

Qy    481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
          ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db   1507 ATATTGAAAGGTGATGATGCCAAAGTTAGCATGGAAGAGAGAGCTGGCCTCACAGTTCCA 1566

Qy    501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
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Db   1567 AGGGCACATAGTCTCGTTTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1626

Qy    521 Ser 521
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Db   1627 TCT 1629
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RESULT 3
AF195806
LOCUS       AF195806               1566 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Vigna radiata isoflavone synthase 1 (ifs1) mRNA, partial cds.
ACCESSION   AF195806
VERSION     AF195806.1  GI:6979535
KEYWORDS    .
SOURCE      Vigna radiata.
  ORGANISM  Vigna radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Vigna.
REFERENCE   1  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
     source          1. .1566
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                     /db_xref="taxon:157791"
     gene            1. .>1566
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                     /note="cytochrome P450"
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                     RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI
                     WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTL
                     LEFAEDETMEIKITKDHIKGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEA
                     YSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGAL
                     ILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEARPLDLRGQHFQLLPFGSGRRMCP
                     GVNLATSGMATLLASLIQCFDLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCV
                     PLARIGVASKLLSK"
BASE COUNT      416 a    394 c    385 g    371 t
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-259       Length:         1566
Score:                  2268.00         Matches:        454
Percent Similarity:     87.14%          Conservative:   0
Best Local Similarity:  87.14%          Mismatches:     67
Query Match:            94.66%          Indels:         0
DB:                     8               Gaps:           0

US-09-857-581-66 (1-521) x AF195806 (1-1566)

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
          ||||||||||||||||||||||||||   ||||||||||||||   ||||||||||||
Db      1 ATGTTGCTGGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 60

Qy     21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
          ||||||   |||   ||||||||||||||||||||||||||||||||||||||   |||
Db     61 ACTCCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 120

Qy     41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
          ||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db    121 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 180

Qy     61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
          ||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db    181 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 240

Qy     81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
          ||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db    241 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 300

Qy    101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
          |||   ||||||||||||||||||||   |||   ||||||||||||      ||||||
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Db     301 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 360

Qy     121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
           |||   ||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db     361 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 420

Qy     141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
           ||||||||||||||||||   ||||||||||||||||||||||||||||||||   |||
Db     421 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 480

Qy     161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
           |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||||
Db     481 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 540

Qy     181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
           ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||
Db     541 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 600

Qy     201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
           ||||||||||||||||||||||||   ||||||||||||||||||||||||||   |||
Db     601 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 660

Qy     221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
           ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 720

Qy     241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
           ||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db     721 GACCCTGTCGTTGAAAGAGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 780

Qy     261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
           ||||||      |||||||||   |||||||||   ||||||||||||||||||||||||
Db     781 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 840

Qy     281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
           ||||||||||||   ||||||||||||||||||      ||||||||||||||||||||||
Db     841 GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCAAGGGTCTTGTTGTCGAC 900

Qy     301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
              ||||||||||||   ||||||||||||      ||||||||||||||||||||||||
Db     901 TTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 960

Qy     321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
           ||||||||||||   ||||||      ||||||||||||   ||||||||||||||||||
Db     961 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGCCTACAGTGTTGTGGGAAAG 1020

Qy     341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
           |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1080

Qy     361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
           ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db    1081 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1140

Qy     381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
              |||||||||   |||   ||||||||||||||      ||||||||||||||||||
Db    1141 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA 1200

Qy     401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
           |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db    1201 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1260

Qy     421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
           |||   ||||||||||||||      ||||||||||||||   ||||||||||||||||
Db    1261 ACAGGGGCTGAAGGGGAAGCAAGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1320

Qy     441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
           ||||||||||||||||||   ||||||||||||||   ||||||||||||||   |||
Db    1321 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1380

Qy     461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 ACACTTCTCGCATCTCTTATTCAGTGCTTTGACTTGCAAGTGCTGGGTCCACAAGGACAG 1440

Qy     481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
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Db    1441 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGCCGGCCTCACTGTTCCA 1500

Qy     501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
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Db    1501 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1560

Qy     521 Ser 521
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Db    1561 TCT 1563
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RESULT 4
AF195807
LOCUS       AF195807               1566 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Vigna radiata isoflavone synthase 2 (ifs2) mRNA, complete cds.
ACCESSION   AF195807
VERSION     AF195807.1  GI:6979537
KEYWORDS    .
SOURCE      Vigna radiata.
  ORGANISM  Vigna radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Vigna.
REFERENCE   1  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
     source          1. .1566
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BASE COUNT      414 a    393 c    387 g    372 t
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-259       Length:         1566
Score:                  2268.00         Matches:        454
Percent Similarity:     87.14%          Conservative:   0
Best Local Similarity:  87.14%          Mismatches:     67
Query Match:            94.66%          Indels:         0
DB:                     8               Gaps:           0

US-09-857-581-66 (1-521) x AF195807 (1-1566)

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
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Db      1 ATGTTGCTGGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 60

Qy     21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
          ||||||   |||   ||||||||||||||||||||||||||||||||||||||   |||
Db     61 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 120

Qy     41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
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Db    121 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCGCTC 180

Qy     61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
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Db    181 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 240

Qy     81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
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Db    241 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 300

Qy    101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
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Db    301 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 360

Qy    121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
                |||   ||||||||||||   ||||||||||||||||||||||||||||||||
Db    361 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 420

Qy    141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
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Db    421 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 480

Qy    161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
          |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||
Db    481 AGGGCTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 540

Qy    181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
          ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||
Db    541 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 600

Qy    201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
          ||||||||||||||||||||||||   ||||||||||||||||||||||||||   |||
Db    601 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 660

Qy    221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 720

Qy    241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
          ||||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db    721 GACCCTGTCGTTGAAAGAGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 780

Qy    261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
          ||||||      |||||||||   |||||||||   ||||||||||||||||||||||||
Db    781 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 840

Qy    281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
          ||||||||||||   ||||||||||||||||||      ||||||||||||||||||||||
Db    841 GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCAAGGGTCTTGTTGTCGAC 900

Qy    301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
              ||||||||||||   ||||||||||||      ||||||||||||||||||||||||
Db    901 TTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 960

Qy    321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
          ||||||||||||   ||||||      ||||||||||||   ||||||||||||||||||
Db    961 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGAAAG 1020

Qy    341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1080

Qy    361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
          ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db   1081 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACGGAAGAGTGT 1140

Qy    381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
              |||||||||   |||   ||||||||||||||      ||||||||||||||||||
Db   1141 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA 1200
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Qy     401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
           |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db    1201 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1260

Qy     421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
           |||   ||||||||||||||||      ||||||||||||||   ||||||||||||||||
Db    1261 ACAGGGGCTGAAGGGGAAGCAAGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1320

Qy     441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
           ||||||||||||||||||   ||||||||||||||||   ||||||||||||||||   |||
Db    1321 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1380

Qy     461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 ACACTTCTTGCATCTCTTATTCAGTGCTTTGACTTGCAAGTGCTGGGTCCACAAGGACAG 1440

Qy     481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
           ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGCCGGCCTCACTGTTCCA 1500

Qy     501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1560

Qy     521 Ser 521
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Db    1561 TCT 1563
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RESULT 5
AF195808
LOCUS       AF195808               1566 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Vigna radiata isoflavone synthase 3 (ifs3) mRNA, complete cds.
ACCESSION   AF195808
VERSION     AF195808.1  GI:6979539
KEYWORDS    .
SOURCE      Vigna radiata.
  ORGANISM  Vigna radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Vigna.
REFERENCE   1  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
     source          1. .1566
                     /organism="Vigna radiata"
                     /db_xref="taxon:157791"
     gene            1. .1566
                     /gene="ifs3"
     CDS             1. .1566
                     /gene="ifs3"
                     /note="cytochrome P450"
                     /codon_start=1
                     /product="isoflavone synthase 3"
                     /protein_id="AAF34529.1"
                     /db_xref="GI:6979540"
                     /translation="MLLELALGLLVLALFLHLRPTPTAKSKALRHLPNPPSPKPRLPF
                     IGHLHLLKDKLLHYALIDLSKKHGPLFSLYFGSMPTVVASTPELFKLFLQTHEATSFN
                     TRFQTSAIRRLTYDSSVAMVPFGPYWKFVRKLIMNDLLNATTVNKLRPLRTQQIRKFL
                     RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI
                     WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTL
                     LEFAEDETTEIKITKDHIKGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEV
                     YSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGAL
                     ILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEARPLDLRGQHFQLLPFGSGRRMCP
                     GVNLATSGMATLLASLIQCFDLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCV
                     PLARIGVASKLLS"
BASE COUNT      415 a    393 c    386 g    372 t
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-259      Length:          1566
Score:                  2268.00        Matches:         454
Percent Similarity:     87.14%         Conservative:    0
Best Local Similarity:  87.14%         Mismatches:      67
Query Match:            94.66%         Indels:          0
DB:                     8              Gaps:            0

US-09-857-581-66 (1-521) x AF195808 (1-1566)

Qy       1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
           ||||||||||||||||||||||||||||   ||||||||||||||   ||||||||||||
Db       1 ATGTTGCTGGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 60

Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
           ||||||   |||   ||||||||||||||||||||||||||||||||||||||   |||
Db      61 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 120

Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db     121 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 180

Qy      61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
           ||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db     181 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 240

Qy      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
           ||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db     241 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 300

Qy     101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
           |||   ||||||||||||||||||||   |||   ||||||||||||      ||||||
Db     301 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 360
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Qy    121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
Db    361 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 420

Qy    141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
Db    421 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 480

Qy    161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
Db    481 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 540

Qy    181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
Db    541 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 600

Qy    201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
Db    601 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 660

Qy    221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
Db    661 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 720

Qy    241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
Db    721 GACCCTGTCGTTGAAAGAGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 780

Qy    261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
Db    781 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 840

Qy    281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
Db    841 GAGGATGAGACCACGGAGATCAAAATCACCAAGGACCACATCAAGGGTCTTGTTGTCGAC 900

Qy    301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
Db    901 TTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 960

Qy    321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
Db    961 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGAAAG 1020

Qy    341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db   1021 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1080

Qy    361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
Db   1081 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1140

Qy    381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
Db   1141 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA 1200

Qy    401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
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Db   1201 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1260

Qy    421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db   1261 ACAGGGGCTGAAGGGGAAGCAAGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1320

Qy    441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db   1321 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1380

Qy    461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
Db   1381 ACACTTCTTGCATCTCTTATTCAGTGCTTTGACTTGCAAGTGCTGGGTCCACAAGGACAG 1440

Qy    481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db   1441 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGGGCCGGCCTCACTGTTCCA 1500

Qy    501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db   1501 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1560

Qy    521 Ser 521
Db   1561 TCT 1563
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RESULT 6
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LOCUS       AF195810               1566 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Trifolium pratense isoflavone synthase 1 (ifs1) mRNA, complete cds.
ACCESSION   AF195810
VERSION     AF195810.1  GI:6979543
KEYWORDS    .
SOURCE      Trifolium pratense.
  ORGANISM  Trifolium pratense
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Trifolium.
REFERENCE   1  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
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                     RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI
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                     LEFAEDETTEIKITKDHIKGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEV
                     YSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGAL
                     ILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEARPLDLRGQHFQLLPFGSGRRMCP
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                     PLARIGVASKLLS"
BASE COUNT      416 a    393 c    387 g    370 t
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-259       Length:         1566
Score:                  2268.00         Matches:        454
Percent Similarity:     87.14%          Conservative:   0
Best Local Similarity:  87.14%          Mismatches:     67
Query Match:            94.66%          Indels:         0
DB:                     8               Gaps:           0

US-09-857-581-66 (1-521) x AF195810 (1-1566)

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
          |||||||||||||||||||||||||||   ||||||||||||||||   ||||||||||||
Db      1 ATGTTGCTGGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 60

Qy     21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
          ||||||   |||   ||||||||||||||||||||||||||||||||||||||   |||
Db     61 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 120

Qy     41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
          ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db    121 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 180

Qy     61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
          |||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db    181 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 240

Qy     81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
          |||||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db    241 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 300

Qy    101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
          |||   ||||||||||||||||||||   |||   ||||||||||||      ||||||
Db    301 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 360

Qy    121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
                |||   ||||||||||||   |||||||||||||||||||||||||||||||||||
Db    361 ATGGTTCCCATCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 420

Qy    141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
          ||||||||||||||||||   ||||||||||||||||||||||||||||||||   |||
Db    421 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 480

Qy    161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
          |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||||
Db    481 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 540

Qy    181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
          ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||
Db    541 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 600

Qy    201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
          |||||||||||||||||||||||||   ||||||||||||||||||||||||||   |||
Db    601 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 660

Qy    221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 720

Qy    241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
          |||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db    721 GACCCTGTCGTTGAAAGAGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 780

Qy    261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
          ||||||      |||||||||   |||||||||   ||||||||||||||||||||||||
Db    781 GGAGAGGTTGATGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 840

Qy    281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
          ||||||||||||   ||||||||||||||||||      ||||||||||||||||||||||
Db    841 GAGGATGAGACCACGGAGATCAAAATCACCAAGGACCACATCAAGGGTCTTGTTGTCGAC 900

Qy    301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
              ||||||||||||   ||||||||||||      ||||||||||||||||||||||||
Db    901 TTTTTCTCGGCAGGGACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 960

Qy    321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
          ||||||||||||   ||||||      ||||||||||||   ||||||||||||||||||||
Db    961 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGAAAG 1020

Qy    341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1080

Qy    361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
          ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db   1081 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1140

Qy    381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
              ||||||||   |||   ||||||||||||||      ||||||||||||||||||
Db   1141 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA 1200

Qy    401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
          |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||
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Db    1201 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1260

Qy     421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
           |||   ||||||||||||||||      ||||||||||||||   ||||||||||||||||
Db    1261 ACAGGGGCTGAAGGGGAAGCAAGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1320

Qy     441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
           ||||||||||||||||||   ||||||||||||||||   ||||||||||||||   |||
Db    1321 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1380

Qy     461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 ACACTTCTTGCATCTCTTATTCAGTGCTTTGACTTGCAAGTGCTGGGTCCACAAGGACAG 1440

Qy     481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
           ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGGGCCGGCCTCACTGTTCCA 1500

Qy     501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1560

Qy     521 Ser 521
           |||
Db    1561 TCT 1563

RESULT 7
AF195811
LOCUS       AF195811                1566 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Trifolium pratense isoflavone synthase 2 (ifs2) mRNA, complete cds.
ACCESSION   AF195811
VERSION     AF195811.1  GI:6979545
KEYWORDS    .
SOURCE      Trifolium pratense.
  ORGANISM  Trifolium pratense
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Trifolium.
REFERENCE   1  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
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                     LEFAEDETTEIKITKDHIKGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEV
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                     ILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEARPLDLRGQHFQLLPFGSGRRMCP
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BASE COUNT      415 a    393 c    386 g    372 t
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-259       Length:         1566
Score:                  2268.00         Matches:        454
Percent Similarity:     87.14%          Conservative:   0
Best Local Similarity:  87.14%          Mismatches:     67
Query Match:            94.66%          Indels:         0
DB:                     8               Gaps:           0

US-09-857-581-66 (1-521) x AF195811 (1-1566)

Qy       1 MetLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
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Db       1 ATGTTGCTGGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 60

Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
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Db      61 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 120

Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db     121 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 180

Qy      61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
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Db     181 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 240

Qy      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
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Db     241 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 300

Qy     101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
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Db     301 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 360

Qy     121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
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Db     361 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 420

Qy     141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
           ||||||||||||||||||   ||||||||||||||||||||||||||||||||   |||
Db     421 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 480

Qy     161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
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Db     481 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 540

Qy     181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
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Qy     201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
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Qy     221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
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Qy     241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
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Qy     281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
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Qy     301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
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Qy     321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
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Qy     361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
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Qy     381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
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Qy     401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
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Db    1201 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1260

Qy     421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
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Qy     441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
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Db    1321 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1380

Qy     461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
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Db    1381 ACACTTCTTGCATCTCTTATTCAGTGCTTTGACTTGCAAGTGCTGGGTCCACAAGGACAG 1440

Qy     481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
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Qy     501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
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Qy     521 Ser 521
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DEFINITION  Vigna radiata isoflavone synthase 4 (ifs4) mRNA, complete cds.
ACCESSION   AF195809
VERSION     AF195809.1  GI:6979541
KEYWORDS    .
SOURCE      Vigna radiata.
  ORGANISM  Vigna radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Vigna.
REFERENCE   1  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1566)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
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BASE COUNT      417 a    392 c    385 g    372 t
ORIGIN

Alignment Scores:
Pred. No.:              1.35e-259       Length:         1566
Score:                  2267.00         Matches:        454
Percent Similarity:     87.14%          Conservative:   0
Best Local Similarity:  87.14%          Mismatches:     67
Query Match:            94.62%          Indels:         0
DB:                     8               Gaps:           0

US-09-857-581-66 (1-521) x AF195809 (1-1566)

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
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Db    121 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 180

Qy     61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
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Db    181 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 240

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Db    241 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 300

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Db    361 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 420

Qy    141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
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Db    421 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 480

Qy    161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
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Db    481 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 540

Qy    181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
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Db    541 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 600

Qy    201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
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Db    601 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 660

Qy    221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
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Db    661 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 720

Qy    241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
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Db    721 GACCCTGTCGTTGAAAGAGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 780

Qy    261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
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Db    781 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 840

Qy    281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
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Db    841 GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCAAGGGTCTTGTTGTCGAC 900

Qy    301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
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Db    901 TTTTTCTCGGCAGGAACAGACTCCACAGCGGAGGCAACAGAGTGGGCATTGGCAGAACTC 960

Qy    321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
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Db    961 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGAAAG 1020

Qy    341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
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Db   1021 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1080

Qy    361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
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Db   1081 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1140

Qy    381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
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Qy    401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
          |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db   1201 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1260
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Qy     421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
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Db    1261 ACAGGGGCTGAAGGGGAAGCAAGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1320

Qy     441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
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Db    1321 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1380

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Db    1381 ACACTTCTTGCATCTCTTATTCAGTGCTTTGACTTGCAAGTGCTGGGTCCACAAGGACAG 1440

Qy     481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
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Qy     521 Ser 521
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Db    1561 TCT 1563
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RESULT 9
AF135484
LOCUS       AF135484               1722 bp    mRNA    linear   PLN 02-AUG-1999
DEFINITION  Glycine max cytochrome P450 monooxygenase CYP93C1v2p (CYP93C1v2)
            mRNA, complete cds.
ACCESSION   AF135484
VERSION     AF135484.1  GI:5059123
KEYWORDS    .
SOURCE      Glycine max.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 1722)
  AUTHORS   Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
  TITLE     Molecular characterization of the enzyme catalyzing the aryl
            migration reaction of isoflavonoid biosynthesis in soybean
  JOURNAL   Arch. Biochem. Biophys. 367 (1), 146-150 (1999)
  MEDLINE   99306846
   PUBMED   10375412
REFERENCE   2  (bases 1 to 1722)
  AUTHORS   Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAR-1999) Plant Biology, Noble Foundation, 2510 Sam
            Noble Pkwy, Ardmore, OK 73402, USA
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                     AF022462; causes change of T to I (aa 156)"
                     /replace="c"
     misc_difference 918
                     /gene="CYP93C1v2"
                     /note="difference compared to GenBank Accession Number
                     AF022462; causes change of E to K (aa 295)"
                     /replace="g"
     misc_difference 1612. .1620
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                     /note="9 bp insertion compared to GenBank Accession Number
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                     /replace=""
BASE COUNT      470 a    422 c    407 g    423 t
ORIGIN

Alignment Scores:
Pred. No.:              1.52e-259      Length:          1722
Score:                  2267.00        Matches:         454
Percent Similarity:     87.14%         Conservative:    0
Best Local Similarity:  87.14%         Mismatches:      67
Query Match:            94.62%         Indels:          0
DB:                     8              Gaps:            0

US-09-857-581-66 (1-521) x AF135484 (1-1722)

Qy       1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
           ||||||||||||||||||||||||||   ||||||||||||||   ||||||||||||
Db      36 ATGTTGCTTGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 95

Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
           ||||||   |||   ||||||||||||||||||||||||||||||||||||||   |||
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Db     96 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 155

Qy     41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
          ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db    156 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 215

Qy     61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
          ||||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db    216 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 275

Qy     81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
          ||||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db    276 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 335

Qy    101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
          |||   ||||||||||||||||||||   |||   ||||||||||||      ||||||
Db    336 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 395

Qy    121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
                |||   ||||||||||||   ||||||||||||||||||||||||||||||||||||
Db    396 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 455

Qy    141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
          ||||||||||||||||||   ||||||||||||||||||||||||||||||||||   |||
Db    456 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTT 515

Qy    161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
          |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||||
Db    516 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 575

Qy    181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
          ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||
Db    576 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 635

Qy    201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
          ||||||||||||||||||||||   ||||||||||||||||||||||||||   |||
Db    636 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 695

Qy    221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 755

Qy    241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
          ||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db    756 GACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 815

Qy    261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
          ||||||      |||||||||   |||||||||   ||||||||||||||||||||||||||
Db    816 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 875

Qy    281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
          ||||||||||||   ||||||||||||||||||      ||||||||||||||||||||||
Db    876 GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCAAGGGTCTTGTTGTCGAC 935

Qy    301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
             ||||||||||||   ||||||||||||      ||||||||||||||||||||||||
Db    936 TTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 995

Qy    321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
          ||||||||||||   ||||||      ||||||||||||   ||||||||||||||||||
Db    996 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGAAAG 1055

Qy    341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1056 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1115

Qy    361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db   1116 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1175

Qy    381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
             |||||||||   |||   ||||||||||||||||      ||||||||||||||||||
Db   1176 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA 1235

Qy    401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
          |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||||
Db   1236 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1295

Qy    421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
          |||   ||||||||||||||||      ||||||||||||||||   ||||||||||||||||
Db   1296 ACAGGGGCTGAAGGGGAAGCAGGGCCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1355

Qy    441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
          ||||||||||||||||||   ||||||||||||||||   ||||||||||||||||   |||
Db   1356 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1415

Qy    461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1416 ACACTTCTTGCATCTCTTATTCAGTGCTTCGACTTGCAAGTGCTGGGTCCACAAGGACAG 1475

Qy    481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
          ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db   1476 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGCCGGCCTCACTGTTCCA 1535

Qy    501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1536 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1595

Qy    521 Ser 521
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Db   1596 TCT 1598
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RESULT 10
AF022462
LOCUS       AF022462               1824 bp    mRNA    linear   PLN 02-MAR-1999
DEFINITION  Glycine max cytochrome P450 monooxygenase CYP93C1p (CYP93C1) mRNA,
            complete cds.
ACCESSION   AF022462
VERSION     AF022462.1  GI:2739005
KEYWORDS    .
SOURCE      Glycine max.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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          Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
          Glycine.
REFERENCE   1  (bases 1 to 1824)
  AUTHORS   Siminszky,B., Corbin,F.T., Ward,E.R., Fleischmann,T.J. and
          Dewey,R.E.
  TITLE     Expression of a soybean cytochrome P450 monooxygenase cDNA in yeast
          and tobacco enhances the metabolism of phenylurea herbicides
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1750-1755 (1999)
  MEDLINE   99145622
   PUBMED   9990096
REFERENCE   2  (bases 1 to 1824)
  AUTHORS   Siminszky,B., Dewey,R.E. and Corbin,F.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-SEP-1997) Crop Science, North Carolina State
          University, Box 7620, Raleigh, NC 27695, USA
FEATURES             Location/Qualifiers
     source          1. .1824
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
     gene            1. .1824
                     /gene="CYP93C1"
     CDS             54. .1619
                     /gene="CYP93C1"
                     /note="cytochrome P450 monooxygenase"
                     /codon_start=1
                     /product="CYP93C1p"
                     /protein_id="AAB94591.1"
                     /db_xref="GI:2739006"
                     /translation="MLLELALGLLVLALFLHLRPTPTAKSKALRHLPNPPSPKPRLPF
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                     RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI
                     WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTL
                     LEFAEDETMEIKITKDHIEGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEV
                     YSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGAL
                     ILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCP
                     GVNLATSGMATLLASLIQCFDLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCV
                     PLARIGVASKLLS"
BASE COUNT      497 a    448 c    416 g    463 t
ORIGIN

Alignment Scores:
Pred. No.:              1.3e-257        Length:         1824
Score:                  2251.00         Matches:        451
Percent Similarity:     86.76%          Conservative:   1
Best Local Similarity:  86.56%          Mismatches:     69
Query Match:            93.95%          Indels:         0
DB:                     8               Gaps:           0

US-09-857-581-66 (1-521) x AF022462 (1-1824)

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
          |||||||||||||||||||||||||||   ||||||||||||||||   ||||||||||||
Db     54 ATGTTGCTTGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 113

Qy     21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
          ||||||   |||   ||||||||||||||||||||||||||||||||||||||||   |||

Db    114 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 173

Qy     41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
          ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db    174 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 233

Qy     61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
          ||||||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db    234 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 293

Qy     81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db    294 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 353

Qy    101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
          |||   ||||||||||||||||||||   |||   ||||||||||||      ||||||
Db    354 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 413

Qy    121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
                |||   ||||||||||||   ||||||||||||||||||||||||||||||||
Db    414 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC 473

Qy    141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
          ||||||||||||||||||   ||||||||||||||||||||||||||   ||||||   |||
Db    474 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGACCCGCAAGTTCCTT 533

Qy    161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
          |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||||
Db    534 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 593

Qy    181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
          ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||
Db    594 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 653

Qy    201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
          ||||||||||||||||||||||||   ||||||||||||||||||||||||||   ||| -
Db    654 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 713

Qy    221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    714 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 773

Qy    241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
          ||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db    774 GACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 833

Qy    261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
          ||||||      |||||||||   |||||||||   ||||||||||||||||||||||||
Db    834 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 893

Qy    281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
          ||||||||||||   ||||||||||||||||||      |||:::||||||||||||||||
Db    894 GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCGAGGGTCTTGTTGTCGAC 953

Qy    301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
             ||||||||||||   ||||||||||||      ||||||||||||||||||||||||
Db    954 TTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 1013
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Qy     321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
           ||||||||||||   ||||||      ||||||||||||   ||||||||||||||||||
Db    1014 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGAAAG 1073

Qy     341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
           |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1074 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1133

Qy     361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
           ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db    1134 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1193

Qy     381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
              |||||||||   |||   ||||||||||||||||      ||||||||||||||||||
Db    1194 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA 1253

Qy     401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
           |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db    1254 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1313

Qy     421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
           |||   ||||||||||||||      ||||||||||||||   ||||||||||||||||
Db    1314 ACAGGGGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1373

Qy     441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
           ||||||||||||||||||   ||||||||||||||   ||||||||||||||   |||
Db    1374 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1433

Qy     461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1434 ACACTTCTTGCATCTCTTATTCAGTGCTTCGACTTGCAAGTGCTGGGTCCACAAGGACAG 1493

Qy     481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
           ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db    1494 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGCCGGCCTCACTGTTCCA 1553

Qy     501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1554 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1613

Qy     521 Ser 521
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Db    1614 TCT 1616
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RESULT 11
AF195799
LOCUS       AF195799               1824 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Glycine max isoflavone synthase 2 (ifs2) mRNA, complete cds.
ACCESSION   AF195799
VERSION     AF195799.1  GI:6979521
KEYWORDS    .
SOURCE      Glycine max.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 1824)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1824)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
     source          1. .1824
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                     /db_xref="taxon:3847"
     gene            1. .1824
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     CDS             54. .1619
                     /gene="ifs2"
                     /codon_start=1
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                     /db_xref="GI:6979522"
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                     TRFQTSAIRRLTYDSSVAMVPFGPYWKFVRKLIMNDLPNATTVNKLRPLRTQQTRKFL
                     RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI
                     WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTL
                     LEFAEDETMEIKITKDHIEGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEV
                     YSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGAL
                     ILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCP
                     GVNLATSGMATLLASLIQCFDLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCV
                     PLARIGVASKLLS"
BASE COUNT      497 a    448 c    416 g    463 t
ORIGIN

Alignment Scores:
Pred. No.:              1.3e-257        Length:         1824
Score:                  2251.00         Matches:        451
Percent Similarity:     86.76%          Conservative:   1
Best Local Similarity:  86.56%          Mismatches:     69
Query Match:            93.95%          Indels:         0
DB:                     8               Gaps:           0

US-09-857-581-66 (1-521) x AF195799 (1-1824)

Qy       1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
           ||||||||||||||||||||||||||   ||||||||||||||   ||||||||||||
Db      54 ATGTTGCTTGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 113

Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
           ||||||   |||   ||||||||||||||||||||||||||||||||||||||   |||
Db     114 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 173
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Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
           ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db     174 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 233

Qy      61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
           ||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db     234 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 293

Qy      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
           ||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db     294 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 353

Qy     101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
           |||   ||||||||||||||||||||   |||   ||||||||||||      ||||||
Db     354 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 413

Qy     121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
                 |||   ||||||||||||   ||||||||||||||||||||||||||||||||
Db     414 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC 473

Qy     141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
           ||||||||||||||||||   ||||||||||||||||||||||||||   ||||||   |||
Db     474 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGACCCGCAAGTTCCTT 533

Qy     161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
           |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||||
Db     534 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 593

Qy     181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
           ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||
Db     594 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 653

Qy     201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
           ||||||||||||||||||||||||   ||||||||||||||||||||||||||   |||
Db     654 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 713

Qy     221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
           ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     714 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 773

Qy     241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
           ||||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db     774 GACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 833

Qy     261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
           ||||||      |||||||||. |||||||||   ||||||||||||||||||||||||
Db     834 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 893

Qy     281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
           ||||||||||||   ||||||||||||||||||      |||:::|||||||||||||||
Db     894 GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCGAGGGTCTTGTTGTCGAC 953

Qy     301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu 320
              ||||||||||||   ||||||||||||      ||||||||||||||||||||||||
Db     954 TTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC 1013

Qy     321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
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           ||||||||||||   ||||||      ||||||||||||   ||||||||||||||||||
Db    1014 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGAAAG 1073

Qy     341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
           |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1074 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACATTAGAGCAATCGTGAAG 1133

Qy     361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
           ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db    1134 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1193

Qy     381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
              |||||||||   |||.  ||||||||||||||||      ||||||||||||||||||
Db    1194 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCAATGTATGGCAAGTA 1253

Qy     401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
           |||   |||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db    1254 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCTGAGAGGTTCCTAGAG 1313

Qy     421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
           |||   ||||||||||||||||      ||||||||||||||   ||||||||||||||||
Db    1314 ACAGGGGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGACAACATTTTCAACTTCTC 1373

Qy     441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
           ||||||||||||||||||   ||||||||||||||||   ||||||||||||||   |||
Db    1374 CCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTTCGGGAATGGCA 1433

Qy     461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1434 ACACTTCTTGCATCTCTTATTCAGTGCTTCGACTTGCAAGTGCTGGGTCCACAAGGACAG 1493

Qy     481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
           ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db    1494 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGCCGGCCTCACTGTTCCA 1553

Qy     501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1554 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1613

Qy     521 Ser 521
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Db    1614 TCT 1616
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RESULT 12
AF195819
LOCUS       AF195819               1902 bp    DNA     linear   PLN 23-MAR-2000
DEFINITION  Glycine max isoflavone synthase 2 (ifs2) gene, complete cds.
ACCESSION   AF195819
VERSION     AF195819.1  GI:7288454
KEYWORDS    .
SOURCE      Glycine max.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 1902)
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  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1902)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, PO Box 80402,
            Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
     source          1. .1902
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                     /db_xref="taxon:3847"
     gene            1. .1902
                     /gene="ifs2"
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                     /gene="ifs2"
                     /product="isoflavone synthase 2"
     CDS             join(52. .948,1085. .1753)
                     /gene="ifs2"
                     /note="cytochrome P450"
                     /codon_start=1
                     /product="isoflavone synthase 2"
                     /protein_id="AAF45143.1"
                     /db_xref="GI:7288455"
                     /translation="MLLELALGLLVLALFLHLRPTPTAKSKALRHLPNPPSPKPRLPF
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                     RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI
                     WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTL
                     LEFAEDETMEIKITKDHIEGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEV
                     YSVVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGAL
                     ILFNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCP
                     GVNLATSGMATLLASLIQCFDLQVLGPQGQILKGGDAKVSMEERAGLTVPRAHSLVCV
                     PLARIGVASKLLS"
BASE COUNT      517 a    455 c    440 g    490 t
ORIGIN

Alignment Scores:
Pred. No.:              1.06e-251       Length:         1902
Score:                  2201.50         Matches:        451
Percent Similarity:     79.72%          Conservative:   1
Best Local Similarity:  79.54%          Mismatches:     69
Query Match:            91.88%          Indels:         46
DB:                     8               Gaps:           1

US-09-857-581-66 (1-521) x AF195819 (1-1902)

Qy       1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
           |||||||||||||||||||||||||||   ||||||||||||||   ||||||||||||
Db      52 ATGTTGCTTGAACTTGCACTTGGTTTATTGGTTTTGGCTCTGTTTCTGCACTTGCGTCCC 111

Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
           ||||||   |||   ||||||||||||||||||||||||||||||||||||||   |||

Db     112 ACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAACCCACCAAGCCCAAAGCCT 171

Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
           ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db     172 CGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAACTTCTCCACTACGCACTC 231

Qy      61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
           ||||||||||||||||||||||||||||||||||||||      ||||||||||||||||||
Db     232 ATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTACTTTGGCTCCATGCCAACC 291

Qy      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
           ||||||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db     292 GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTCCAAACGCACGAGGCAACTTCC 351

Qy     101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
           |||   ||||||||||||||||||||||   |||   ||||||||||||      ||||||
Db     352 TTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC 411

Qy     121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
                 |||   ||||||||||||   ||||||||||||||||||||||||||||||||
Db     412 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC 471

Qy     141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
           ||||||||||||||||||   ||||||||||||||||||||||||   ||||||   |||
Db     472 AACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAACAGACCCGCAAGTTCCTT 531

Qy     161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
           |||   |||||||||   |||||||||   ||||||||||||   ||||||||||||||||
Db     532 AGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTTGACCGAGGAGCTTCTG 591

Qy     181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
           ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||
Db     592 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC 651

Qy     201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
           ||||||||||||||||||||||||   ||||||||||||||||||||||||||||   |||
Db     652 ATCGCTCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 711

Qy     221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
           ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     712 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTTGAACAAGTTC 771

Qy     241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
           ||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db     772 GACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC 831

Qy     261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
           ||||||      |||||||||   |||||||||   ||||||||||||||||||||||||
Db     832 GGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGACACTTTGCTTGAATTCGCT 891

Qy     281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValVal--- 299
           ||||||||||||   ||||||||||||||||      |||:::||||||||||||
Db     892 GAGGATGAGACCATGGAGATCAAAATCACCAAGGACCACATCGAGGGTCTTGTTGTCGTG 951

Qy     299 ------------------------------------------------------------ 299

Db     952 AGTTTCCTGCTTCATTCATTGATCGAAATATGCAGTATTTTGTTAACAAGAGATCGAGAA 1011
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Qy     299 ------------------------------------------------------------ 299

Db    1012 TTGACATTTATATATTCATGTGGTGGCAATTAATTAACGGTACGCATTCTTAATCGATAT 1071

Qy     300 ------------Asp***PheSerAlaGly***AspSerThrAla******ThrGluTr 315
                       |||   ||||||||||||   ||||||||||||      ||||||||
Db    1072 TGTGTATGTGCAGGACTTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTG 1131

Qy     315 pAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu******AlaArgGluGlu***Ty 335
           ||||||||||||||||||||||||||||   ||||||      ||||||||||||   ||
Db    1132 GGCATTGGCAGAACTCATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTA 1191

Qy     335 rSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIl 355
           ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db    1192 CAGTGTTGTGGGAAAGGACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTACAT 1251

Qy     355 eArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLy 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1252 TAGAGCAATCGTGAAGGAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAA 1311

Qy     375 sCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu******Ph 395
           ||||   |||||||||   ||||||||   |||   ||||||||||||||      ||
Db    1312 GTGCACAGAAGAGTGTGAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTT 1371

Qy     395 eAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPr 415
           ||||||||||||||||||   |||   ||||||||||||||||||||||   |||||
Db    1372 CAATGTATGGCAAGTAGGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCC 1431

Qy     415 oGluArgPheLeuGluThr***AlaGluGlyGluAla******LeuAspLeuArgGly** 435
           ||||||||||||||||||   ||||||||||||||      ||||||||||||||
Db    1432 TGAGAGGTTCCTAGAGACAGGGGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGACA 1491

Qy     435 *HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAl 455
            ||||||||||||||||||||||||||||||||   ||||||||||||||   |||||
Db    1492 ACATTTTCAACTTCTCCCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGC 1551

Qy     455 aThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLe 475
           ||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db    1552 TACTTCGGGAATGGCAACACTTCTTGCATCTCTTATTCAGTGCTTCGACTTGCAAGTGCT 1611

Qy     475 uGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAl 495
           ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db    1612 GGGTCCACAAGGACAGATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGC 1671

Qy     495 aGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyVa 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1672 CGGCCTCACTGTTCCAAGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCGT 1731

Qy     515 lAlaSerLysLeuLeuSer 521
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Db    1732 TGCATCTAAACTCCTTTCT 1750

RESULT 13
AF195818
LOCUS       AF195818               1800 bp    DNA     linear   PLN 23-MAR-2000
DEFINITION  Glycine max isoflavone synthase 1 (ifs1) gene, partial cds.
ACCESSION   AF195818
VERSION     AF195818.1  GI:7288452
KEYWORDS    .
SOURCE      Glycine max.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 1800)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1800)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, PO Box 80402,
            Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:3847"
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                     /gene="ifs1"
     mRNA            join(<1. .893,1112. .>1800)
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                     /note="cytochrome P450"
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                     /product="isoflavone synthase 1"
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                     /db_xref="GI:7288453"
                     /translation="LELALGLFVLALFLHLRPTPSAKSKALRHLPNPPSPKPRLPFIG
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                     VVGKDRLVDEVDTQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGALVL
                     FNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCPGV
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BASE COUNT      476 a    441 c    413 g    470 t
ORIGIN

Alignment Scores:
Pred. No.:              3.04e-250      Length:          1800
Score:                  2189.00        Matches:         451
Percent Similarity:     76.18%         Conservative:    0
Best Local Similarity:  76.18%         Mismatches:      68
Query Match:            91.36%         Indels:          74
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DB: 8 Gaps: 1

US-09-857-581-66 (1-521) x AF195818 (1-1800)

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Qy      3 LeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro 22
          |||||||||||||||||||||   ||||||||||||||||   ||||||||||||||||||
Db      3 CTGGAACTTGCACTTGGTTTGTTTGTGTTAGCTTTGTTTCTGCACTTGCGTCCCACACCA 62

Qy     23 ***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***ProArgLeu 42
            |||   ||||||||||||||||||||||||||||||||||||||   |||||||||
Db     63 AGTGCAAAATCAAAAGCACTTCGCCACCTCCCAAACCCTCCAAGCCCAAAGCCTCGTCTT 122

Qy     43 ProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAsp 62
          ||||||||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db    123 CCCTTCATTGGCCACCTTCACCTCTTAAAAGATAAACTTCTCCACTATGCACTCATCGAT 182

Qy     63 LeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThrValVal 82
          |||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db    183 CTCTCCAAAAAGCATGGCCCCTTATTCTCTCTCCTTCGGCTCCATGCCAACCGTCGTT 242

Qy     83 AlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSerPhe*** 102
          ||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db    243 GCCTCCACCCCTGAGTTGTTCAAGCTCTTCCTCCAAACCCACGAGGCAACTTCCTTCAAC 302

Qy    103 ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla****** 122
          ||||||||||||||||||||   |||   ||||||||||||      ||||||
Db    303 ACAAGGTTCCAAACCTCTGCCATAAGACGCCTCACTTACGACAACTCTGTGGCCATGGTT 362

Qy    123 Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAla 142
          |||   ||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db    363 CCATTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTCAACGCC 422

Qy    143 ThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg*** 162
          ||||||||||||   ||||||||||||||||||||||||||||||||   ||||||
Db    423 ACCACCGTCAACAAGCTCAGGCCTTTGAGGACCCAACAGATCCGCAAGTTCCTTAGGGTT 482

Qy    163 MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp 182
          |||||||||   |||||||||   ||||||||||||   ||||||||||||||||||||
Db    483 ATGGCCCAAAGCGCAGAGGCCCAGAAGCCCCTTGACGTCACCGAGGAGCTTCTCAAATGG 542

Qy    183 ***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAspIleAla 202
            |||||||||   |||||||||   ||||||||||||||||||||||||||||||||||
Db    543 ACCAACAGCACCATCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGACATCGCT 602

Qy    203 ArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys 222
          ||||||||||||||||   ||||||||||||||||||||||||||||   |||||||||
Db    603 CGCGAGGTTCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTGGCCTTTGAAG 662

Qy    223 ***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspPro 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    663 TATCTCAAGGTTGGAAAGTATGAGAAGAGGATTGATGACATCTTGAACAAGTTCGACCCT 722

Qy    243 ValValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu 262
          ||||||||||||||||||||||||||||||   ||||||||||||||   |||||||||
Db    723 GTCGTTGAAAGGGTCATCAAGAAGCGCCGTGAGATCGTCAGAAGGAGAAAGAACGGAGAA 782

Qy    263 ******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAsp 282
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Db    783 GTTGTTGAGGGCGAGGCCAGCGGCGTCTTCCTCGACACTTTGCTTGAATTCGCTGAGGAC 842

Qy    283 GluThr***GluIleLysIleThrLys******IleLysGlyLeuValVal--------- 299
          ||||||   ||||||||||||||||||      ||||||||||||||||
Db    843 GAGACCATGGAGATCAAAATTACCAAGGAGCAAATCAAGGGCCTTGTTGT-CGTAAGTTT 901

Qy    299 ------------------------------------------------------------ 299

Db    902 CCTTCTTCTCTCCTACTTTATTACTTTCTTTCATTCATCATATGTATTGGCATTAAATAG 961

Qy    299 ------------------------------------------------------------ 299

Db    962 TATACTATATGAGAAAATATGTTACGCACTCACGGTGTAAAGATATGTGGTGTTTTTTTA 1021

Qy    299 ------------------------------------------------------------ 299

Db   1022 AAAAGAGATACAGAAGTTGCTTTTATGCATGTATGTTAACGTATATTTACTCAAGTGGAA 1081

Qy    300 ------------------------------Asp***PheSerAlaGly***AspSerThr 309
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Db   1082 ACTAATTAATTCTCAATTTTGGGTATGTAGGACTTTTTCTCTGCAGGGACAGATTCCACA 1141

Qy    310 Ala******ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu****** 329
          |||      ||||||||||||||||||||||||||||||||||||   ||||||
Db   1142 GCGGTGGCAACAGAGTGGGCATTGGCAGAGCTCATCAACAATCCCAGGGTGTTGCAAAAG 1201

Qy    330 AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThr 349
          ||||||||||||   ||||||||||||||||||||||   ||||||||||||||||||||
Db   1202 GCTCGTGAGGAGGTCTACAGTGTTGTGGGCAAAGATAGACTCGTTGACGAAGTTGACACT 1261

Qy    350 GlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeu 369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1262 CAAAACCTTCCTTACATTAGGGCCATTGTGAAGGAGACATTCCGAATGCACCCACCACTC 1321

Qy    370 ProValValLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGlu 389
          ||||||||||||||||||||   |||||||||   |||||||||   |||   ||||||
Db   1322 CCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGTGAGATTAATGGGTATGTGATCCCAGAG 1381

Qy    390 GlyAlaLeu******PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArg 409
          |||||||||      ||||||||||||||||||||||   |||   ||||||||||||||||
Db   1382 GGAGCATTGGTTCTTTTCAATGTTTGGCAAGTAGGAAGGGACCCCAAATACTGGGACAGA 1441

Qy    410 ProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla****** 429
          |||||||||   ||||||||||||||||||||||||   ||||||||||||||||
Db   1442 CCATCAGAATTCCGTCCCGAGAGGTTCTTAGAAACTGGTGCTGAAGGGGAAGCAGGGCCT 1501

Qy    430 LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCys 449
          ||||||||||||||   ||||||||||||||||||||||||||||||||||   ||||||
Db   1502 CTTGATCTTAGGGGCCAGCATTTCCAACTCCTCCCATTTGGGTCTGGGAGGAGAATGTGC 1561

Qy    450 ProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCys 469
          |||||||||   ||||||||||||||   ||||||||||||||||||||||||||||||
Db   1562 CCTGGTGTCAATTTGGCTACTTCAGGAATGGCAACACTTCTTGCATCTCTTATCCAATGC 1621

Qy    470 PheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysVal 489
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Db   1622 TTTGACCTGCAAGTGCTGGGCCCTCAAGGACAAATATTGAAAGGTGATGATGCCAAAGTT 1681

Qy    490 SerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1682 AGCATGGAAGAGAGAGCTGGCCTCACAGTTCCAAGGGCACATAGTCTCGTTTGTGTTCCA 1741

Qy    510 LeuAlaArgIleGlyValAlaSerLysLeuLeuSer 521
          |||||||||||||||||||||||||||||||||||
Db   1742 CTTGCAAGGATCGGCGTTGCATCTAAACTCCTTTCT 1777

RESULT 14
AF195801
LOCUS       AF195801               1501 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Medicago sativa isoflavone synthase 2 (ifs2) mRNA, partial cds.
ACCESSION   AF195801
VERSION     AF195801.1  GI:6979525
KEYWORDS    .
SOURCE      Medicago sativa.
  ORGANISM  Medicago sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 1501)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1501)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:3879"
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                     SSVAMAPFGPYWKFVRKLIMNDLLNATTVNKLRPLRTQQIRKFLRVMAQGAEAQKPLD
                     LTEELLKWTNSTTSMMMLGEAEEIRDIARERVLKIFGEYSLTDFIRPLKHLKVGKYEKR
                     IDDILNKFDPVVERVIKKRREIVRRRKNGEVVEGEVSGVFLDTLLEFAEDETTEIKIT
                     KDHIKGLVVDFFSAGTDSTAVATEWALAELINNPKVLEKAREEVYSVVGKDRLVDEVD
                     TQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGALILFNVWQVGRDSKY
                     WDRPSEFRPERFLETGAEGEARPLDLRGQHFQLLPFGSGRRMCPGVNLATSGMATLLA
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BASE COUNT      404 a    382 c    373 g    342 t
ORIGIN

Alignment Scores:
Pred. No.:              1.26e-249       Length:         1501
Score:                  2183.00         Matches:        433
Percent Similarity:     86.77%          Conservative:   0
Best Local Similarity:  86.77%          Mismatches:     66
Query Match:            91.11%          Indels:         0
DB:                     8               Gaps:           0

US-09-857-581-66 (1-521) x AF195801 (1-1501)

Qy     15 Phe***HisLeuArgProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsn 34
          |||  ||||||||||||||||||  |||  ||||||||||||||||||||||||||||
Db      3 TTTCTGCACTTGCGTCCCACACCCACTGCAAAATCAAAAGCACTTCGCCATCTCCCAAAC 62

Qy     35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
          ||||||||||||  ||||||||||||||||||||||||  ||||||||||||||||||
Db     63 CCACCAAGCCCAAAGCCTCGTCTTCCCTTCATAGGACACCTTCATCTCTTAAAAGACAAA 122

Qy     55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer****** 74
          ||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db    123 CTTCTCCACTACGCACTCATCGACCTCTCCAAAAAACATGGTCCCTTATTCTCTCTCTAC 182

Qy     75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    183 TTTGGCTCCATGCCAACCGTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTTCCTTCAA 242

Qy     95 ******GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
                ||||||||||||||||  ||||||||||||||||||||  |||  ||||||
Db    243 ACGCACGAGGCAACTTCCTTCAACACAAGGTTCCAAACCTCAGCCATAAGACGCCTCACC 302

Qy    115 TyrAsp******ValAla******Pro***GlyProTyrTrp***PheValArgLysLeu 134
          ||||||      ||||||      |||  ||||||||||||  ||||||||||||||||
Db    303 TATGATAGCTCAGTGGCCATGGCTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTC 362

Qy    135 IleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThrGln 154
          ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db    363 ATCATGAACGACCTTCTCAACGCCACCACTGTAAACAAGTTGAGGCCTTTGAGGACCCAA 422

Qy    155 GlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp 174
          ||||||||||||  ||||||  |||||||||  |||||||||  ||||||||||||
Db    423 CAGATCCGCAAGTTCCTTAGGGTTATGGCCCAAGGCGCAGAGGCACAGAAGCCCCTTGAC 482

Qy    175 ***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGlu 194
             ||||||||||||||||||||  |||||||||  |||||||||  |||||||||
Db    483 TTGACCGAGGAGCTTCTGAAATGGACCAACAGCACCACCTCCATGATGATGCTCGGCGAG 542

Qy    195 AlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyrSerLeu 214
          ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db    543 GCTGAGGAGATCAGAGACATCGCCCGCGAGGTTCTTAAGATCTTTGGCGAATACAGCCTC 602

Qy    215 ThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAsp 234
          ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||||
Db    603 ACTGACTTCATCCGGCCATTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGAC 662
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Qy     235 AspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***Ile 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db     663 GACATCTTGAACAAGTTCGACCCTGTCGTTGAAAGAGTCATCAAGAAGCGCCGTGAGATC 722

Qy     255 ValArgArgArg***AsnGlyGlu******GluGlyGlu***SerGlyVal***LeuAsp 274
           ||||||||||||  |||||||||      |||||||||  |||||||||  ||||||
Db     723 GTGAGGAGGAGAAAGAACGGAGAGGTTGTTGAGGGTGAGGTCAGCGGGGTTTTCCTTGAC 782

Qy     275 ThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys******Ile 294
           ||||||||||||||||||||||||||||||  ||||||||||||||||||      |||
Db     783 ACTTTGCTTGAATTCGCTGAGGATGAGACCACGGAGATCAAAATCACCAAGGACCACATC 842

Qy     295 LysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla******ThrGlu 314
           ||||||||||||||||||  ||||||||||||  ||||||||||||      ||||||
Db     843 AAGGGTCTTGTTGTCGACTTTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAG 902

Qy     315 TrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu******AlaArgGluGlu*** 334
           ||||||||||||||||||||||||||||||||  ||||||      ||||||||||||
Db     903 TGGGCATTGGCAGAACTCATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTC 962

Qy     335 TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyr 354
           ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db     963 TACAGTGTTGTGGGAAAGGACAGACTTGTGGACGAAGTTGACACTCAAAACCTTCCTTAC 1022

Qy     355 IleArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArg 374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1023 ATTAGAGCAATCGTGAAGGAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGA 1082

Qy     375 LysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu****** 394
           ||||||  |||||||||  |||  ||||||||||||||||
Db    1083 AAGTGCACAGAAGAGTGTGAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTC 1142

Qy     395 PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***Arg 414
           ||||||||||||||||||||  |||  ||||||||||||||||||||||||  |||
Db    1143 TTCAATGTATGGCAAGTAGGAAGAGACTCCAAATACTGGGACAGACCATCGGAGTTCCGT 1202

Qy     415 ProGluArgPheLeuGluThr***AlaGluGlyGluAla******LeuAspLeuArgGly 434
           ||||||||||||||||||||  ||||||||||||||||      ||||||||||||||||
Db    1203 CCTGAGAGGTTCCTAGAGACAGGGGCTGAAGGGGAAGCAAGGCCTCTTGATCTTAGGGGA 1262

Qy     435 ***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***Leu 454
              ||||||||||||||||||||||||||||||||  ||||||||||||||  |||
Db    1263 CAACATTTTCAACTTCTCCCATTTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTG 1322

Qy     455 AlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal 474
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db    1323 GCTACTTCGGGAATGGCAACACTTCTTGCATCTCTTATTCAGTGCTTTGACTTGCAAGTG 1382

Qy     475 LeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArg 494
           ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db    1383 CTGGGTCCACAAGGACAGATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGG 1442

Qy     495 AlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle 513
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Db    1443 GCCGGCCTCACTGTTCCAAGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATC 1499

RESULT 15
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AF195800
LOCUS       AF195800               1501 bp    mRNA    linear   PLN 16-FEB-2000
DEFINITION  Medicago sativa isoflavone synthase 1 (ifs1) mRNA, partial cds.
ACCESSION   AF195800
VERSION     AF195800.1  GI:6979523
KEYWORDS    .
SOURCE      Medicago sativa.
  ORGANISM  Medicago sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 1501)
  AUTHORS   Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
            McGonigle,B.
  TITLE     Identification and expression of isoflavone synthase, the key
            enzyme for biosynthesis of isoflavones in legumes
  JOURNAL   Nat. Biotechnol. 18 (2), 208-212 (2000)
  MEDLINE   20124255
   PUBMED   10657130
REFERENCE   2  (bases 1 to 1501)
  AUTHORS   Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box
            80402, Wilmington, DE 19880-0402, USA
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                     VTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFIWPLKYLKVGKYEKR
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                     KEQIKGLVVDLFSAGTDSTAVATEWALAELINNPRVLQKAREEVYSVVGKDRLVDEVD
                     TQNLPYIRAIVKETFRMHPPLPVVKRKCTEECEINGYVIPEGALVLFNVWQVGRDPKY
                     WDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCPGVNLATSGMATLLA
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BASE COUNT      390 a    400 c    366 g    345 t
ORIGIN

Alignment Scores:
Pred. No.:              2.86e-249       Length:         1501
Score:                  2180.00         Matches:        433
Percent Similarity:     86.77%          Conservative:   0
Best Local Similarity:  86.77%          Mismatches:     66
Query Match:            90.98%          Indels:         0
DB:                     8               Gaps:           0
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US-09-857-581-66 (1-521) x AF195800 (1-1501)

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Qy      15 Phe***HisLeuArgProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsn 34
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Db       3 TTTCTGCACTTGCGTCCCACACCAAGTGCAAAATCAAAAGCACTTCGCCACCTCCCAAAC 62

Qy      35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
           ||||||||||||  ||||||||||||||||||||||||  ||||||||||||||||||||
Db      63 CCCCCAAGCCCAAAGCCTCGTCTTCCCTTCATTGGCCACCTTCACCTCTTAAAAGATAAA 122

Qy      55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer****** 74
           ||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db     123 CTTCTCCACTATGCACTCATCGATCTCTCCAAAAAGCATGGCCCCTTATTCTCTCTCTCC 182

Qy      75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
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Db     183 TTCGGCTCCATGCCAACCGTCGTTGCCTCCACCCCTGAGTTGTTCAAGCTCTTCCTCCAA 242

Qy      95 ******GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
                 ||||||||||||||||  ||||||||||||||||||||  |||  ||||||
Db     243 ACCCACGAGGCAACTTCCTTCAACACAAGGTTCCAAACCTCTGCCACAAGACGCCTCACT 302

Qy     115 TyrAsp******ValAla******Pro***GlyProTyrTrp***PheValArgLysLeu 134
           ||||||      ||||||      |||  ||||||||||||  ||||||||||||||||
Db     303 TACGACAACTCTGTGGCCATGGTTCCATTCGGACCTTACTGGAGGTTCGTGAGGAAGCTC 362

Qy     135 IleMetAsnAspLeuLeuAsnAlaThrThrValAsn***LeuArgProLeuArgThrGln 154
           ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db     363 ATCATGAACGACCTTCTCAACGCCACCACCGTCAACAAGCTCAGGCCTTTGAGGACCCAA 422

Qy     155 GlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp 174
           ||||||||||||  ||||||  |||||||||  |||||||||  ||||||||||||||
Db     423 CAGATCCGCAAGTTCCTTAGGGTTATGGCCCAAAGCGCAGAGGCCCAGAAGCCCCTTGAC 482

Qy     175 ***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGlu 194
               ||||||||||||||||||||  |||||||||  |||||||||  |||||||||
Db     483 GTCACCGAGGAGCTTCTCAAATGGACCAACAGCACCATCTCCATGATGATGCTCGGCGAG 542

Qy     195 AlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyrSerLeu 214
           ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db     543 GCTGAGGAGATCAGAGACATCGCTCGCGAGGTTCTTAAGATCTTCGGCGAATACAGCCTC 602

Qy     215 ThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIleAsp 234
           ||||||||||||  |||||||||  ||||||||||||||||||||||||||||||||||
Db     603 ACTGACTTCATCTGGCCTTTGAAGTATCTCAAGGTTGGAAAGTATGAGAAGAGGATTGAT 662

Qy     235 AspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***Ile 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db     663 GACATCTTGAACAAGTTCGACCCTGTCGTTGAAAGGGTCATCAAGAAGCGCCGTGGGATC 722

Qy     255 ValArgArgArg***AsnGlyGlu******GluGlyGlu***SerGlyVal***LeuAsp 274
           ||||||||||||  |||||||||      |||||||||  |||||||||  ||||||
Db     723 GTCAGAAGGAGAGAGAACGGAGAAGTTGTTGAGGGCGAGGCCAGCGGCGTCTTCCTCGAC 782

Qy     275 ThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys******Ile 294
           ||||||||||||||||||||||||||||||  ||||||||||||||||||      |||
Db     783 ACTTTGCTTGAATTCGCTGAGGACGAGACCATGGAGATCAAAATTACCAAGGAGCAAATC 842

Qy     295 LysGlyLeuValValAsp***PheSerAlaGly***AspSerThrAla******ThrGlu 314
           ||||||||||||||||||  ||||||||||||  ||||||||||||      ||||||
Db     843 AAGGGCCTTGTTGTCGACCTTTTCTCTGCAGGGACAGATTCCACAGCGGTGGCAACAGAG 902

Qy     315 TrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu******AlaArgGluGlu*** 334
           ||||||||||||||||||||||||||||||  ||||||      ||||||||||||
Db     903 TGGGCATTGGCAGAGCTCATCAACAATCCCAGGGTGTTGCAAAAGGCTCGTGAGGAGGTC 962

Qy     335 TyrSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyr 354
           ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db     963 TACAGTGTTGTGGGCAAAGATAGACTCGTTGACGAAGTTGACACTCAAAACCTTCCTTAC 1022

Qy     355 IleArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArg 374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1023 ATTAGGGCCATTGTGAAGGAGACATTCCGAATGCACCCACCACTCCCAGTGGTCAAAAGA 1082

Qy     375 LysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu****** 394
           ||||||  |||||||||  |||||||||  |||  ||||||||||||||||
Db    1083 AAGTGCACAGAAGAGTGTGAGATTAATGGGTATGTGATCCCAGAGGGAGCATTGGTTCTT 1142

Qy     395 PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***Arg 414
           ||||||||||||||||||||  |||  ||||||||||||||||||||||||  |||
Db    1143 TTCAATGTTTGGCAAGTAGGAAGGGACCCCAAATACTGGGACAGACCATCCGAATTCCGT 1202

Qy     415 ProGluArgPheLeuGluThr***AlaGluGlyGluAla******LeuAspLeuArgGly 434
           ||||||||||||||||||||  ||||||||||||||||      ||||||||||||||||
Db    1203 CCCGAGAGGTTCTTAGAAACTGGTGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGC 1262

Qy     435 ***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***Leu 454
               ||||||||||||||||||||||||||||||||  ||||||||||||||||  |||
Db    1263 CAGCATTTCCAACTCCTCCCATTTGGGTCTGGGAGGAGAATGTGCCCTGGTGTCAATTTG 1322

Qy     455 AlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal 474
           ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db    1323 GCTACTTCAGGAATGGCAACACTTCTTGCATCTCTTATCCAATGCTTTGACCTGCAAGTG 1382

Qy     475 LeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArg 494
           ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db    1383 CTGGGCCCTCAAGGACAAATATTGAAAGGTGATGATGCCAAAGTTAGCATGGAAGAGAGA 1442

Qy     495 AlaGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIle 513
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1443 GCTGGCCTCACAGTTCCAAGGGCACATAGTCTCGTTTGTGTTCCACTTGCAAGGATC 1499
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Search completed: May 18, 2003, 13:07:12
Job time : 2876 secs

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 18, 2003, 07:48:03 ; Search time 239 Seconds
(without alignments)